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(54) Title: ANTIGENIC POLYPEPTIDES

(57) Abstract: The invention relates to a method for the identification of antigenic polypeptides expressed by pathogenic microbes; vaccines comprising said polypeptides; recombinant methods to manufacutre said polypeptides; and therapeutic antibodies directed to said polypeptides.

Antigenic Polypeptides

The invention relates to a method for the identification of antigenic polypeptides expressed by pathogenic microbes; vaccines comprising said polypeptides; recombinant methods to manufacture said polypeptides; and therapeutic antibodies directed to said polypeptides.

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Microbial organisms cause a number of fatal or debilitating diseases which affect many millions of people around the world. Currently methods to control microbial organisms include the use of antimicrobial agents (antibiotics) and disinfectants. These have proved to be problematic since exposure to these agents places a significant selection pressure resulting in the creation of resistant microbes which can avoid the effects of the antimicrobial agent(s). For example, recently it has been discovered that microbial organisms have become resistant to triclosan, an agent added to many disinfectants used in households and industrial environments.

An arguably greater problem is the evolution of antibiotic resistant strains of a number of significant pathogenic microbes.

For example, and not by way of limitation, it is estimated that there are up to 50 million people world-wide infected with drug resistant tuberculosis (TB) (Figures from the World Health Organisation, 1998). In the past the use of antibiotics to treat TB relied on the administration of single drugs (eg ethionamide) which promoted a relatively high frequency of resistance. For this reason, combinations of drugs are now used to treat tuberculosis. However the fatality rate in cases caused by strains that are resistant to at least one drug used to treat tuberculosis still approaches 50% even when treatment is given. Mycobacterium tuberculosis, the causative agent of TB, is a slow growing bacteria and takes a long time to kill. Therefore, for a drug combination to be effective a person with TB must take the drug combination daily for at least six months. Accordingly, patients frequently have to take two or more pills daily and this requires a regimented dosage over a relatively long period of

treatment. Many patients take the medications only intermittently and therefore do not finish the full course of therapy to completely eradicate the *M. tuberculosis* infection. Moreover, TB is strongly associated with HIV infection and therefore the establishment of TB is strongly correlated with immunosuppression.

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Vaccination against TB has been available for many years. The bacillus calmette and guerin (BCG) vaccination has been widely used throughout the world for a long time because it is a safe and inexpensive means to vaccinate large numbers of people who potentially could contract TB. BCG is derived from live, attenuated strains of *Mycobacterium bovis*. However the impact of vaccination on the infectious forms of TB is minimal and BCG has therefore contributed little to the overall control of the disease.

A further example of a pathogenic organism which has developed resistance to antibiotics is Staphylococcus aureus. S.aureus is a bacterium whose normal habitat is the epithelial lining of the nose in about 20-40% of normal healthy people and is also commonly found on people's skin usually without causing harm. However, in certain circumstances, particularly when skin is damaged, this germ can cause infection. This is a particular problem in hospitals where patients may have surgical procedures and/or be taking immunosuppressive drugs. These patients are much more vulnerable to infection with S.aureus because of the treatment they have received. Resistant strains of S.aureus have arisen in recent years. Methicillin resistant strains are prevalent and many of these resistant strains are also resistant to several other antibiotics. Currently there is no effective vaccination procedure for S. aureus. In the US, S.aureus infections are the cause of 13% of the two million hospitalised infections each year. This represents 260,000 people with an infection of S.aureus, of which 60-80,000 die.

S. aureus is therefore a major human pathogen capable of causing a wide range of life threatening diseases including septicaemia, endocarditis, arthritis and toxic shock. This ability is determined by the versatility of the organism and its arsenal of

components involved in virulence. Pathogenicity is multifactorial and no one component has shown to be responsible for a particular infection, see Projan, S.J. & Novick, R.P. (1997) in The Staphylococci in Human Disease (Crossley, K.B. & Archer, G.L., eds.) pp.55-81.

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At the onset of infection, and as it progresses, the needs and environment of the organism changes and this is mirrored by a corresponding alteration in the virulence determinants which *S. aureus* produces. At the beginning of infection it is important for the pathogen to adhere to host tissues and so a large repertoire of cell surface associated attachment proteins are made. These include collagen-, fibrinogen- and fibronectin-binding proteins. The pathogen also has the ability to evade host defences by the production of factors that reduce phagocytosis or interfere with the ability of the cells to be recognised by circulating antibodies.

Often a focus of infection develops as an abscess and the number of organisms increases. S. aureus has the ability to monitor its own cell density by the production of a quorum sensing peptide. Accumulation of the peptide, associated with physiological changes brought about by the beginning of starvation of the cells, elicits a switch in virulence determinant production from adhesins to components involved in invasion and tissue penetration. These include a wide range of hemolysins, proteases and other degradative enzymes.

During the process of any infection the virulence determinants made by *S. aureus* are produced in response to environmental and physiological stimuli. These stimuli will be dependent on the niche within the body and will change as the infection progresses. Little is known of the conditions *in vivo* and it is likely that some components are produced solely in this environment. These are therefore potential vaccine components, which could not be discovered by previous techniques.

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One of the most important developments in recent medical history is the development of vaccines which provide prophylactic protection from a wide variety of pathogenic organisms. Many vaccines are produced by inactivated or attenuated pathogens which are injected into an individual. The immunised individual responds by producing both a humoral (antibody) and cellular (cytolytic T cells, CTL's) response. For example, hepatitis vaccines are made by heat inactivating the virus and treating it with a cross linking agent such as formaldehyde. An example of an attenuated pathogen useful as a vaccine is represented by polio vaccines which are produced by attenuating a live pathogen.

However the use of attenuated organisms in vaccines for certain diseases is problematic due to the lack of knowledge regarding the pathology of the condition and the nature of the attenuation. For certain viral agents this is a particular problem since viruses, in particular retroviruses, have an error prone replication cycle which results viable mutations in the genes which comprise the virus. This can result in alterations to antigenic determinants which have previously been used as vaccines. An alternative to the use of inactivated or attenuated pathogens is the identification of pathogen epitopes to which the immune system is particularly sensitive. In this regard many pathogenic toxins produced by pathogenic organisms during an infection are particularly useful in the development of vaccines which protect the individual from a particular pathogenic organism.

The development of so-called subunit vaccines (vaccines in which the immunogen is a fragment or subunit of a protein or complex expressed by a particular pathogenic organism) has been the focus of considerable medical research. The need to identify candidate molecules useful in the development of subunit vaccines is apparent not least because conventional chemotherapeutic approaches to the control of pathogenic organisms has more recently been stymied by the development of antibiotic resistance. A number of methods have been developed to identify potential antigenic polypeptides which can be used as a vaccine. One such method is disclosed herein.

It has been known for many years that tumour cells produce a number of tumour cell specific antigens, some of which are presented at the tumour cell surface. The immune system recognises these antigens as foreign thereby resulting in the production of antibodies to self antigens, so called autoantibodies or autologous antisera.

One such technique is <u>Serological</u> identification of antigens by <u>recombinant</u> <u>Expression Cloning</u>, abbreviated to SEREX.

Typically, the technique involves the extraction of RNA from tumour tissue followed by the selective enrichment of mRNA from the isolated total RNA. The mRNA is reverse transcribed into cDNA using viral reverse transcriptase. The cDNA thus synthesised is subcloned into an expression vector and transformed into an appropriate bacterial strain. The transformed bacteria are plated onto a suitable nutrient agar and under appropriate growth conditions the subcloned cDNA is expressed from the expression vector in the bacterial cell. The cells are lysed naturally by the use of phage based expression vectors, for example λ phage or phagemid based vectors, which through their lytic cycle cause cell lysis. The released polypeptides are transferred to a suitable membrane support (i.e. nitrocellulose, nylon) and exposed to autologous antisera from the patient from which the tumour tissue was originally isolated. The immunoscreening methodology allows the identification of genes that are over expressed or inappropriately expressed in a selected tumour tissue from a patient.

We have exploited this techinque to identify antigenic polypeptides expressed by pathogenic organisms during an infection. Autologous antisera produced during the infection is used to screen an expression library created from genomic DNA to identify and clone antigens.

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In its broadest aspect the invention relates to the identification of antigenic polypeptides expressed during an infection by a pathogenic microbe.

According to a first aspect of the invention there is provided a method to identify antigenic polypeptides comprising:

- (i) providing a nucleic acid library encoding genes or partial gene sequences of a pathogenic organism;
- 10 (ii) transforming/transfecting said library into a host cell;
 - (iii) providing conditions conducive to the expression of said transformed/transfected genes or partial gene sequences;
- 15 (iv) contacting the polypeptides expressed by the genes/partial gene sequences with autologous antisera derived from an animal infected with, or has been infected with, said pathogenic organism; and
- (v) purifying the nucleic acid encoding the polypeptide or partial polypeptide
 binding to said autologous antisera.

In a preferred method of the invention said library comprises genomic DNA of a pathogenic organism.

25 Ideally said pathogenic organism is bacterial.

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More preferably still said bacterial organism is selected from the following:

Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis;

Mycobacterium tuberculsis; Streptococcus group B; Streptoccocus pneumoniae;

Helicobacter pylori; Neisseria gonorrhea; Streptococcus group A; Borrelia

burgdorferi; Coccidiodes immitis; Histoplasma sapsulatum; Neisseria meningitidis type B; Shigella flexneri; Escherichia coli; Haemophilus influenzae.

Preferably still said pathogenic organism is of the genus *Staphylococcus spp.* Ideally organism is *Staphylococcus aureus* or *Staphylococcus epidermidis*.

In a further preferred embodiment of the invention said nucleic acid library is a lambda library, ideally a lambda expression library.

- According to a second aspect of the invention there is provided a nucleic acid molecule comprising a DNA sequence selected from:
 - (i) the DNA sequence as represented in SEQ ID NO's 1-13;
- 15 (ii) DNA sequences which hybridise to the sequence presented in the SEQ ID No's 1-13 identified in (i) above which encode a polypeptide expressed by a pathogenic organism and
- (iii) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (i) and (ii).

In a yet still further preferred embodiment of the invention said nucleic acid molecule is genomic DNA.

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In a preferred embodiment of the invention there is provided an isolated nucleic acid molecule which anneals under stringent hybridisation conditions to the sequences presented in SEQ ID NO's 1-13.

30 Stringent hybridisation/washing conditions are well known in the art. For example, nucleic acid hybrids that are stable after washing in 0.1xSSC, 0.1% SDS at 60°C. It

is well known in the art that optimal hybridisation conditions can be calculated if the sequences of the nucleic acid is known. For example, hybridisation conditions can be determined by the GC content of the nucleic acid subject to hybridisation. Please see Sambrook et al (1989) Molecular Cloning; A Laboratory Approach. A common formula for calculating the stringency conditions required to achieve hybridisation between nucleic acid molecules of a specified homology is:

$$T_m = 81.5^{\circ} C + 16.6 \text{ Log } [\text{Na}^+] + 0.41 [\% G + C] - 0.63 (\% \text{formamide}).$$

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According to a third aspect of the invention there is provided at least one polypeptide identified by the method according to the invention.

In a preferred embodiment of the invention, said polypeptide is associated with infective pathogenicity of an organism according to any previous aspect or embodiment of the invention.

More preferably still said polypeptide is at least one, or part of SEQ ID NO's: 14-19.

According to a fourth aspect of the invention there is provided a nucleic acid molecule characterised in that said nucleic acid molecule is part of a vector adapted to facilitate recombinant expression of the polypeptide encoded by said nucleic acid molecule.

In a preferred embodiment of the invention said vector is an expression vector adapted for prokaryotic gene expression. Alternatively said expression vector is adapted for eukaryotic gene expression.

Typically said adaptation includes, by example and not by way of limitation, the provision of transcription control sequences (promoter sequences) which mediate cell specific expression. These promoter sequences may be cell specific, inducible or constitutive.

Promoter is an art recognised term and, for the sake of clarity, includes the following features which are provided by example only, and not by way of limitation. Enhancer elements are *cis* acting nucleic acid sequences often found 5' to the transcription initiation site of a gene (enhancers can also be found 3' to a gene sequence or even located in intronic sequences and is therefore position independent). Enhancers function to increase the rate of transcription of the gene to which the enhancer is linked. Enhancer activity is responsive to *trans* acting transcription factors (polypeptides) which have been shown to bind specifically to enhancer elements. The binding/activity of transcription factors (please see Eukaryotic Transcription Factors, by David S Latchman, Academic Press Ltd, San Diego) is responsive to a number of environmental cues which include, by example and not by way of limitation, intermediary metabolites (eg glucose, lipids), environmental effectors (eg light, heat,).

- Promoter elements also include so called TATA box and RNA polymerase initiation selection (RIS) sequences which function to select a site of transcription initiation. These sequences also bind polypeptides which function, *inter alia*, to facilitate transcription initiation selection by RNA polymerase.
- 20 Adaptations also include the provision of selectable markers and autonomous replication sequences which both facilitate the maintenance of said vector in either the eukaryotic cell or prokaryotic host. Vectors which are maintained autonomously are referred to as episomal vectors.
- 25 Adaptations which facilitate the expression of vector encoded genes include the provision of transcription termination/polyadenylation sequences. This also includes the provision of internal ribosome entry sites (IRES) which function to maximise expression of vector encoded genes arranged in bicistronic or multi-cistronic expression cassettes.

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These adaptations are well known in the art. There is a significant amount of published literature with respect to expression vector construction and recombinant DNA techniques in general. Please see, Sambrook et al (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory, Cold Spring Harbour, NY and references therein; Marston, F (1987) DNA Cloning Techniques: A Practical Approach Vol III IRL Press, Oxford UK; DNA Cloning: F M Ausubel et al, Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (1994).

- According to yet a further aspect of the invention there is provided a method for the production of the polypeptides according to any previous aspect or embodiment of the invention comprising:
- (i) providing a cell transformed/transfected with a vector according to the invention;
 - (ii) growing said cell in conditions conducive to the manufacture of said polypeptides; and
- 20 (iii) purifying said polypeptide from said cell, or its growth environment.

In a preferred method of the invention said vector encodes, and thus said recombinant polypeptide is provided with, a secretion signal to facilitate purification of said polypeptide.

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According to a fifth aspect of the invention there is provided a cell or cell-line transformed or transfected with the vector according to the invention.

In a preferred embodiment of the invention said cell is a prokaryotic cell.

Alternatively said cell is a eukaryotic cell selected from: fungal, insect, amphibian; mammalian; plant.

According to a yet further aspect of the invention there is provided a vaccine comprising at least one polypeptide according to the invention.

5 Ideally said vaccine further comprises a carrier and/or adjuvant.

The terms adjuvant and carrier are construed in the following manner. Some polypeptide or peptide antigens contain B-cell epitopes but no T cell epitopes. Immune responses can be greatly enhanced by the inclusion of a T cell epitope in the polypeptide/peptide or by the conjugation of the polypeptide/peptide to an immunogenic carrier protein such as key hole limpet haemocyanin or tetanus toxoid which contain multiple T cell epitopes. The conjugate is taken up by antigen presenting cells, processed and presented by human leukocyte antigens (HLA's) class II molecules. This allows T cell help to be given by T cell's specific for carrier derived epitopes to the B cell which is specific for the original antigenic polypeptide/peptide. This can lead to increase in antibody production, secretion and isotype switching.

An adjuvant is a substance or procedure which augments specific immune responses to antigens by modulating the activity of immune cells. Examples of adjuvants include, by example only, agonsitic antibodies to co-stimulatory molecules, Freunds adjuvant, muramyl dipeptides, liposomes. An adjuvant is therefore an immunomodulator. A carrier is an immunogenic molecule which, when bound to a second molecule augments immune responses to the latter.

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In yet a further aspect of the invention there is provided a method to immunise an animal against a pathogenic microbe comprising administering to said animal at least one polypeptide, or part thereof, according to the invention or the vaccine according to the invention.

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In a preferred method of the invention said animal is human.

Preferably the vaccine, or antigenic polypeptide, can be delivered by direct injection either intravenously, intramuscularly, subcutaneously. Further still, the vaccine or antigenic polypeptide, may be taken orally.

Preferably the vaccine is against the bacterial species Staphylococcus aureus.

5 The vaccine may also be against the bacterial species Staphylococcus epidermidis.

It will also be apparent that vaccines or antigenic polypeptides are effective at preventing or alleviating conditions in animals other than humans, for example and not by way of limitation, family pets, livestock, horses.

According to a further aspect of the invention there is provided an antibody, or at least an effective binding part thereof, which binds at least one polypeptide according to the invention.

In a preferred embodiment of the invention said antibody is a polyclonal or monoclonal antibody wherein said antibody is specific to said polypeptide.

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Alternatively, said antibody is a chimeric antibody produced by recombinant methods to contain the variable region of said antibody with an invariant or constant region of a human antibody.

In a further alternative embodiment of the invention, said antibody is humanised by recombinant methods to combine the complimentarity determining regions of said antibody with both the constant (C) regions and the framework regions from the variable (V) regions of a human antibody.

Preferably said antibody is provided with a marker including a conventional label or tag, for example a radioactive and/or fluorescent and/or epitope label or tag.

Preferably said humanised monoclonal antibody to said polypeptide is produced as a fusion polypeptide in an expression vector suitably adapted for transfection or transformation of prokaryotic or eukaryotic cells.

Antibodies, also known as immunoglobulins, are protein molecules which have specificity for foreign molecules (antigens). Immunoglobulins (Ig) are a class of structurally related proteins consisting of two pairs of polypeptide chains, one pair of light (L) (low molecular weight) chain (κ or λ), and one pair of heavy (H) chains (γ , α , μ , δ and ϵ), all four linked together by disulphide bonds. Both H and L chains have regions that contribute to the binding of antigen and that are highly variable from one Ig molecule to another. In addition, H and L chains contain regions that are non-variable or constant.

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The L chains consist of two domains. The carboxy-terminal domain is essentially identical among L chains of a given type and is referred to as the "constant" (C) region. The amino terminal domain varies from L chain to L chain and contributes to the binding site of the antibody. Because of its variability, it is referred to as the "variable" (V) region.

The H chains of Ig molecules are of several classes, α , μ , σ , α , and γ (of which there are several sub-classes). An assembled Ig molecule consisting of one or more units of two identical H and L chains, derives its name from the H chain that it possesses. Thus, there are five Ig isotypes: IgA, IgM, IgD, IgE and IgG (with four sub-classes based on the differences in the H chains, i.e., IgG1, IgG2, IgG3 and IgG4). Further detail regarding antibody structure and their various functions can be found in, Using Antibodies: A laboratory manual, Cold Spring Harbour Laboratory Press.

25 Chimeric antibodies are recombinant antibodies in which all of the V-regions of a mouse or rat antibody are combined with human antibody C-regions. Humanised antibodies are recombinant hybrid antibodies which fuse the complimentarity determining regions from a rodent antibody V-region with the framework regions from the human antibody V-regions. The C-regions from the human antibody are also used. The complimentarity determining regions (CDRs) are the regions within the N-terminal domain of both the heavy and light chain of the antibody to where the

majority of the variation of the V-region is restricted. These regions form loops at the surface of the antibody molecule. These loops provide the binding surface between the antibody and antigen.

Antibodies from non-human animals provoke an immune response to the foreign antibody and its removal from the circulation. Both chimeric and humanised antibodies have reduced antigenicity when injected to a human subject because there is a reduced amount of rodent (i.e. foreign) antibody within the recombinant hybrid antibody, while the human antibody regions do not illicit an immune response. This results in a weaker immune response and a decrease in the clearance of the antibody. This is clearly desirable when using therapeutic antibodies in the treatment of human diseases. Humanised antibodies are designed to have less "foreign" antibody regions and are therefore thought to be less immunogenic than chimeric antibodies.

15 In another aspect of the invention there is provided a vector which is adapted for the expression of the humanised or chimeric antibodies according to the invention.

In a yet further aspect of the invention, there is provided a cell or cell line which has been transformed or transfected with the vector encoding the humanised or chimeric antibody according to the invention.

In a yet further aspect of the invention there is provided a method for the production of the humanised or chimeric antibody according to the invention comprising:

- (i) providing a cell transformed or transfected with a vector which comprises a nucleic acid molecule encoding the humanised or chimeric antibody according to the invention;
- (ii) growing said cell in conditions conducive to the manufacture of said antibody; and
- (iii) purifying said antibody from said cell, or its growth environment.

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In a yet further aspect of the invention there is provided a hybridoma cell line which produces a monoclonal antibody as hereinbefore described.

In a further aspect of the invention there is provided a method of producing monoclonal antibodies according to the invention using hybridoma cell lines according to the invention.

In a further aspect of the invention there is provided a method for preparing a hybridoma cell-line producing monoclonal antibodies according to the invention comprising the steps of:

- i) immunising an immunocompetent mammal with an immunogen comprising at least one polypeptide having the amino acid sequence as represented in SEO. ID No 14-19, or fragments thereof;
- ii) fusing lymphocytes of the immunised immunocompetent mammal with myeloma cells to form hybridoma cells;
- iii) screening monoclonal antibodies produced by the hybridoma cells of step (ii) for binding activity to the amino acid sequences of (i);
- iv) culturing the hybridoma cells to proliferate and/or to secrete said monoclonal antibody; and
- 20 v) recovering the monoclonal antibody from the culture supernatant.

Preferably, the said immunocompetent mammal is a mouse. Alternatively, said immunocompetent mammal is a rat.

The production of monoclonal antibodies using hybridoma cells is well-known in the art. The methods used to produce monoclonal antibodies are disclosed by Kohler and Milstein in Nature 256, 495-497 (1975) and also by Donillard and Hoffman, "Basic Facts about Hybridomas" in Compendium of Immunology V.II ed. by Schwartz, 1981, which are incorporated by reference.

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In a further aspect of the invention there is provided the use of the antibodies for manufacture of a medicament for the treatment of *Staphylococcus aureus*-associated septicaemia, food-poisoning or skin disorders.

In another aspect of the invention there is provided the use of the antibodies according to the invention for the manufacture of a medicament for the treatment of *Staphylococcus epidermidis*-associated septicaemia, peritonitis or endocarditis.

It will be apparent that the polypeptides identified by the method according to the invention will facilitate the production of therapeutic antibodies to a range of diseases resulting from pathogenic infection, for example, septicaemia; tuberculosis; bacteria-associated food poisoning; blood infections; peritonitis; endocarditis; sepsis; meningitis; pneumonia; stomach ulcers; gonorrhoea; strep throat; streptococcal-associated toxic shock; necrotizing fasciitis; impetigo; histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis.

As has already been stated earlier, microbial organisms cause a wide variety of diseases. Listed below, and not by way of limitation, are a number of microorganisms and some of the diseases they cause.

Micro-organism	Disease(s) caused				
Staphylococcus aureus	Sepsis, food poisoning, septicaemia,				
Staphylococcus epidermidis	Peritonitis, septicaemia, endocarditis, other hospital-associated diseases				
Enterococcus faecalis	Endocarditis, cystitis, wound infections				
Mycobacterium tuberculosis	Tuberculosis				
Streptococcus group B	Sepsis, meningitis, pneumonia, bladder infections				
Streptococcus pneumoniae Pneumonia, meningitis					
Helicobacter pylori	Stomach ulcers				
Neisseria gonorrhoea	Gonorrhoea				
Streptococcus group A	Strep throat, necrotizing fasciitis, impetigo, Strep. Toxic shock syndrome				
Borrelia burgdoferi	Lyme disease				
Coccidiodes immitis	Pneumonia				

Histoplasma sapsulatum	Histoplasmosis, pneumonia			
Neisseria meningitidis type B	Meningitis			
Shigella flexneri	Gastro-enteritis, shigellosis, dysentry			
Escherichia coli	Food-poisoning, gastro-enteritis			
Haemophilus influenzae	Meningitis, pneumonia, arthritis, cellulitis			

An embodiment of the invention will now be described by example only and with reference to the following materials, methods and SEQ ID NO's 1-19 and Table 1.

Materials and Methods

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A \(\lambda ZAP\) Express library of genomic DNA of S. aureus 8325/4 was used. It contains fragments of 2-10kb from a partial Sau3A digest of total genomic DNA. This was cloned into the BamH1 site of the vector. The library contains >10x coverage of the genome. The library was probed by plaque lift using an initial screen of approximately 20,000 plaque forming units on a 9cm diameter Petri dish. The plating cells used, their treatment, the plating procedure and buffers were exactly as described in the manufacturers handbook (Stratagene). Plating cells, Escherichia coli XL1-Blue MRF', were infected with phage and plated in 3 ml top LB agar containing 10 mM MgSO₄ onto LB plates containing 10 mM MgSO₄. The plates were then incubated at 42°C for 4 hr. An 8.5cm diameter nitrocellulose filter disc (previously soaked in 10 mM IPTG and air-dried) was placed on each plate and its location marked. The plates were then incubated for a further 3.5 hr at 37°C. The filters were removed and washed in TBST buffer before blocking overnight at 4°C in TBST containing 6% w/v dried skimmed milk and 3% v/v pig serum (Sigma). The serum was used to block any Protein A clones on the filter. The filters are then treated with patient serum (1/5000 dilution) in blocking solution for 90 min at room temperature. Antisera have been obtained from patients convalescing from major S. aureus infections. The filters are then washed for 3x10 min in TBST. Secondary antibody used was goat anti-human whole IgG alkaline phosphatase linked (Sigma)

at 1/30,000 dilution in blocking solution at room temperature for 30 min. The filters were then washed as above and developed using a standard colorimetric procedure.

Cross-reactive plaques were located on the agar plates and cored into 0.2ml phage buffer with 0.02 ml chloroform. The titre of each core stock was determined and the phage plated at approximately 200 plaques per plate. A plaque lift and screen was performed as above to give single, pure cross-reactive clones.

The pure clones were then spotted (1µl) onto plates to give a confluent plaque of 0.5cm diameter. 30 individual clones can be spotted on each plate. A plaque lift is performed and the filter probed with an appropriate sera. In this way clones can be tested for their cross-reactivity with other patient sera, non-infected donor sera and anti-Protein A sera.

Individual clones were then excised to give a phagemid in E. coli XLOLR using the manufacturers protocol (Stratagene). A plasmid miniprep of each was carried out and the size of the genomic insert determined by restriction mapping. The identity of the cloned insert was determined by DNA sequencing using primers against vector sequence, which allows sequencing across the insert. By comparison of the derived sequence against the public domain databases the nature of the cloned gene(s) can be determined.

Hybridisation Solutions/Conditions

Typically, hybridisation conditions uses 4 – 6 x SSPE (20x SSPE contains 175.3g NaCl, 88.2g NaH₂PO₄ H₂O and 7.4g EDTA dissolved to 1 litre and the pH adjusted to 7.4); 5-10x Denhardts solution (50x Denhardts solution contains 5g Ficoll (type 400, Pharmacia), 5g polyvinylpyrrolidone abd 5g bovine serum albumen; 100μg-1.0mg/ml sonicated salmon/herring DNA; 0.1-1.0% sodium dodecyl sulphate; optionally 40-60% deionised formamide. Hybridisation temperature will vary

depending on the GC content of the nucleic acid target sequence but will typically be between 42^{0} - 65^{0} C.

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Staphylococcus aureus clones identified in human sera screen TABLE 1

Patient Sera	Patient Sera Clone Encoded proteins		Locus
			number
A	11	γ hemolysin B and C subunit	1
A	3	Atl	2
A	4	γ hemolysin B and C subunit	1
A	5	γ hemolysin B and C subunit	1
A	7	Novel putative protease (ORF1 novel	7
	8	antigen like) Novel nuclease (YisK)	5
A	9	Novel autolysin	6
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F	5	Novel hemolysin (YjfD)	11

CLAIMS

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An isolated nucleic acid molecule comprising a DNA sequence selected from
 the group consisting of:

- (i) the DNA sequence as represented in SEQ ID NO's 1-13;
- (ii) DNA sequences which hybridise to the sequence presented in the SEQ

 ID No's 1-13 identified in (i) above and which encode a polypeptide expressed by a pathogenic organism; and
 - (iii) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (i) and (ii).
 - 2. An isolated nucleic acid molecule according to claim 1 which is genomic DNA.
- An isolated nucleic acid molecule according to claim 1 or 2 which anneals
 under stringent hybridisation conditions to the sequences presented in SEQ ID
 NO's 1-13.
 - 4. A vector comprising a nucleic acid molecule according to any of claims 1-3.
- 25 5. A vector according to claim 4 wherein the vector is adapted for recombinant expression of the polypeptide encoded by the nucleic acid.
 - A vector according to claim 4 or 5 wherein said vector is an expression vector adapted for prokaryotic gene expression.
 - 7. A vector according to claim 4 or 5 wherein said vector is an expression vector adapted for eukaryotic gene expression.

8. A vector according to any of claims 4 to 7 wherein the adaptation of the vector includes the provision of promoter sequences.

- 5 9. A vector according to claim 8 wherein the promoter sequences provide for cell specific, inducible or constitutive expression.
 - 10. A method to identify antigenic polypeptides comprising:
- 10 (i) providing a nucleic acid library encoding genes or partial gene sequences of a pathogenic organism;
 - (ii) transforming/transfecting said library into a host cell;
- 15 (iii) contacting the polypeptides expressed by the genes/partial gene sequences with autologous antisera derived from an animal infected with, or has been infected with, said pathogenic organism; and
- (iv) purifying the nucleic acid encoding the polypeptide or partial polypeptide
 binding to said autologous antisera.
 - A method according to claim 10 wherein said library comprises genomic DNA of a pathogenic organism.
- 25 12. A method according to claim 10 or claim 11 wherein said pathogenic organism is bacterial.
- 13. A method according to any of claims 10 to 12 wherein said bacterial organism is selected from the following: Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; Mycobacterium tuberculsis; Streptococcus group B; Streptoccocus pneumoniae; Helicobacter pylori;

Neisseria gonorrhea; Streptococcus group A; Borrelia burgdorferi; Coccidiodes immitis; Histoplasma sapsulatum; Neisseria meningitidis type B; Shigella flexneri; Escherichia coli; Haemophilus influenzae

- 5 14. A method according to any of claim 13 wherein said pathogenic organism is Staphylococcus aureus.
 - 15. A method according to any of claim 13 wherein said pathogenic organism is Staphylococcus epidermidis.
- 16. A method according to any of claims 10 to 15 wherein said nucleic acid library is a lambda library.

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- 17. A polypeptide identified by the method according to any of claims 10 to 16.
- 18. A polypeptide according to claim 17 which is selected from the group consisting of SEQ ID NO's: 14-19.
- 19. A method for the production of the polypeptides according to any of claims
 20 17 or 18 comprising:
 - (i) providing a cell transformed/transfected with a vector according to any of claims 4 to 9 and with cell culture conditions; and
 - (ii) purifying said polypeptide from said cell, or its growth environment.
- 25 20. A method according to claim 19 wherein said vector encodes, and thus said recombinant polypeptide is provided with, a secretion signal to facilitate purification of said polypeptide.
- 21. A cell transformed or transfected with the vector according to any of claims 4 to 9.

- 22. A cell according to claim 21 which is a prokaryotic cell.
- 23. A cell according to claim 21 which is a eukaryotic cell selected from the group consisting of: fungal cell, insect cell, amphibian cell; mammalian cell; plant cell.
- 24. A vaccine comprising at least one polypeptide according to claims 16 or 17.
- 25. A vaccine according to claim 24 which further comprises a carrier and/or adjuvant.
 - 26. A method to immunise an animal against a pathogenic microbe comprising administering to the animal at least one polypeptide, or part thereof, according to any previous claim or the vaccine of any previous claim.

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- 27. A method according to claim 26 wherein the animal is human.
- 28. A method according to claim 26 or 27 wherein the vaccine, or antigenic polypeptide, is delivered by direct injection either intravenously, intramuscularly or subcutaneously.
 - 29. A method according to claim 25 or 26 wherein the vaccine or antigenic polypeptide is taken orally.
 - 30. A method according to any of claims 26 to 29 wherein the vaccine is against the bacterial genus *Staphylococcus spp*.
- 25 31. A method according to claim 30 wherein the vaccine is against the bacterial species Staphylococcus aureus.
 - 32. A method according to claim 30 wherein the vaccine is against the bacterial species *Staphylococcus epidermidis*.

33. An antibody, or at least an effective part thereof, which binds at least with a selective part of the polypeptide according to claim 16 or 17.

34. An antibody according to claim 33 which is a monoclonal antibody.

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- 35. An antibody according to claim 33 or 34 wherein said effective part comprises FAb fragments.
- 36. An antibody according to any of claims 33 to 35 which is a chimeric antibody.
 - 37. An antibody according to any of claims 33 to 35 which is a humanised antibody.
- 15 38. An antibody according to any of claims 33 to 37 wherein said antibody is provided with a marker, label or tag.
- An antibody according to claim 38 wherein said antibody is provided with a marker selected from a group consisting of: a radioactive label, a fluorescent label; an epitope tag.
 - 40. An antibody according to any of claims 34 to 39 which is produced as a fusion polypeptide.
- 25 41. A vector which is adapted for the expression of the antibodies according to any of claims 34-40.
 - 42. A cell which has been transformed or transfected with the vector according to claim 41.

43. A method for the production of the antibody according to any of claims 34 or 40 comprising:

- i) providing a cell transformed or transfected with the vector according to claim 41 and with cell culture conditions; and
- 5 ii) purifying said antibody from said cell, or its growth environment.
 - 44. A hybridoma cell line which produces an antibody according to claim 34.
- Use of the antibodies according to any of claims 33 to 40 for the manufacture of a medicament for the treatment of *Staphylococcus aureus*-associated septicaemia, food-poisoning or skin disorders.
 - 46. Use of the antibodies according to any of claims 33 to 40 for the manufacture of a medicament for the treatment of *Staphylococcus epidermidis*-associated septicaemia, peritonitis or endocarditis

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- 47. A method for preparing a hybridoma cell-line producing monoclonal antibodies according to claim 34, comprising the steps of:
 - i) immunising an immunocompetent mammal with an immunogen comprising at least one polypeptide having the amino acid sequence as set forward in SEQ ID No: 14-19, or fragments thereof;
 - ii) fusing lymphocytes of the immunised immunocompetent mammal with myeloma cells to form hybridoma cells;
 - iii) screening monoclonal antibodies produced by the hybridoma cells of step (ii) for binding activity to the amino acid sequences of (i);
 - iv) culturing the hybridoma cells to proliferate and/or to secrete said monoclonal antibody; and
 - v) recovering the monoclonal antibody from the culture supernatant.
- 30 48. A method according to claim 47, wherein said immunocompetent mammal is a mouse

49. A method according to claim 47, wherein said immunocompetent mammal is a rat

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25	Ala	Thr	Lys 435	Gln	Gln	Gln	Ile	Asp 440	ГÀЗ	Ser	Ile	Tyr	Leu 445	Phe	Gly	Thr
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10	ГЛЗ	Glu 690	Gln	Val	Ile	Asn	Gly 695	Gln	Thr	Trp	Tyr	Tyr 700	Gly	Lys	Leu	Ser
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Trp Asn Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro 310 315 Lys Arg His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp 5 Gln His Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly 345 10 Ser Ile Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn Ala Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr 375 15 Gly Lys ' 385 20 <210> 17 <211> 325 <212> PRT <213> Staphylococcus aureus 25 <400> 17 Met Lys Met Asn Lys Leu Val Lys Ser Ser Val Ala Thr Ser Met Ala Leu Leu Leu Ser Gly Thr Ala Asn Ala Glu Gly Lys Ile Thr Pro 30 Val Ser Val Lys Lys Val Asp Asp Lys Val Thr Leu Tyr Lys Thr Thr 35 Ala Thr Ala Asp Ser Asp Lys Phe Lys Ile Ser Gln Ile Leu Thr Phe Asn Phe Ile Lys Asp Lys Ser Tyr Asp Lys Asp Thr Leu Val Leu Lys 40 Ala Thr Gly Asn Ile Asn Ser Gly Phe Val Lys Pro Asn Pro Asn Asp Tyr Asp Phe Ser Lys Leu Tyr Trp Gly Ala Lys Tyr Asn Val Ser Ile 45 105 Ser Ser Gln Ser Asn Asp Ser Val Asn Val Val Asp Tyr Ala Pro Lys 120 50 Asn Gln Asn Glu Glu Phe Gln Val Gln Asn Thr Leu Gly Tyr Thr Phe 135 Gly Gly Asp Ile Ser Ile Ser Asn Gly Leu Ser Gly Gly Leu Asn Gly 55 Asn Thr Ala Phe Ser Glu Thr Ile Asn Tyr Lys Gln Glu Ser Tyr Arg 165 Thr Thr Leu Ser Arg Asn Thr Asn Tyr Lys Asn Val Gly Trp Gly Val 60 Glu Ala His Lys Ile Met Asn Asn Gly Trp Gly Pro Tyr Gly Arg Asp 200

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. •	His	Arg	Gln	Asp 260	Gly	Ala	Lys	Lys	Ser 265	Lys	Ile	Thr	Val	Thr 270	Tyr	Gln
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	Gly	Ala 290	Asn	Tyr	ГÀЗ	Asn	Phe 295	Lys	Thr	Arg	Thr	Phe 300	Lys	Ser	Thr	Tyr
20	Glu 305	Ile	Asp	Trp	Glu	Asn 310	His	Lys	Val	Lys	Leu 315	Leu	Asp	Thr	Lys	Glu 320
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در	Ser	Glu	Val	Glu 20	Gln	Gln	Asn	Ser	Lys 25	Ser	Val	Leu	Trp	Gly 30	Val	Lys
10				20					25							
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	Ala Asp	Asn Leu 50	Ser 35 Phe	20 Phe Val	Ala Gly	Thr Tyr	Glu Lys 55	Ser 40 Pro	25 Gly His	Gln Ser	Lys Lys	Ser Asp 60	Ala 45 Pro	30 Phe	Asp Asp	Ser Tyr
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10 15	Ala Asp Phe 65 Pro	Asn Leu 50 Val Ser Glu	Ser 35 Phe Pro Phe	20 Phe Val Asp Ile Glu 100	Ala Gly Ser Ala 85 Ile	Thr Tyr Glu 70 Thr	Glu Lys 55 Leu Val	Ser 40 Pro Pro Ser Gly	25 Gly His Pro His Arg 105	Gln Ser Leu Glu 90 Asn	Lys Lys Val 75 Lys Met	Ser Asp 60 Gln Gly Asp	Ala 45 Pro Ser Ser	30 Phe Arg Gly Ser	Asp Phe Asp 95 His	Ser Tyr Asn 80 Thr
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30	Ile	Thr	Arg 115	Leu	Val	Tyr	Pro	11e 120	Ile	Asn	Ile	Суз	Val 125	Ile	Val	Phe
	Arg	Pro 130	Ile	Thr	Leu	Leu	Leu 135	Asn	Lys	Leu	Thr	Asp 140	Ser	Ile	Asn	Arg
35	Ser 145	Leu	Ser	ГÀз	Gly	Gln 150	Pro	Gln	Glu	His	Gln 155	Phe	Ser	Lys	Glu	Glu 160
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40	Ile	Glu	Thr	Ser 180	Arg	Leu	Glu	Gly	Val 185	Ile	Asn	Phe	Glu	Asn 190	Leu	Lys
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·	Ser	Asn 210	Ala	Thr	Tyr	Glu	Glu 215	Val	Tyr	Glu	Thr	Val 220	Met	Asn	Lys	Pro
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,	Ser	Leu	Lys	Glu 100	Tyr	Arg	Lys	Tyr	Tyr 105	Glu	Pro	Leu	Ile	Arg 110	Lys	Asn
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	Tyr	Ala 130	Ala	Asn	Thr	qeA	Ala 135	Val	Ala	Thr	Leu	Phe 140	Ser	Thr	Lys	ГЛЗ
15	Asn 145	Phe	Thr	Lys	Asp	Asn 150	Thr	Val	Asp	Asp	Val 155	Ile	Glu	Leu	Ser	Asp 160
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	Arg	Asp	Leu	Lys 100	Gln	Pro	Val	Ile	Leu 105	Asn	Gln	Gln	Phe	Gly 110	Leu	Gly
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	Pro	Asn	Pro 195	Phe	His	Leu	Ile	Tyr 200	Ser	Ile	Leu	Ser	Lys 205	His	Gln	Ser
10	Ala	Ser 210	Ile	Pro	Asp	Asp	Leu 215	Lys	Phe	Glu	Lys	Asp 220	Ile	Ala	Gln	Ile
15	Glu 225	Asp	Ser	Ser	Arg	Pro 230	Asn	Val	Asn	Ile	Ser 235	Ile	Val	туr	Phe	Glu 240
13	Asp	Val	Ser	Thr	Glu 245	Thr	Ile	Leu	Asp	Asn 250	Asp	Glu	Tyr	Arg	Ser 255	Val
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30	Glu 305	Glu	Ser	Gly	Thr	Ser 310	Tyr	Glu	Arg	Val	Arg 315	Gln	Tyr	Arg	Ile	Gly 320
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- 20 Gln Gln Asn His Thr Leu Asp Phe Gln Glu Gln Val Arg Lys Ala Val 50 55 60
- Val Ala Ala Glu Asp Ser Gly Lys Ala Glu Asp Tyr Lys Ile Ser Phe 65 70 75 80
- Asn Asp Ile Glu Phe Leu Pro Pro Val Thr Pro Pro Asn Asn Val Ile 85 90 95
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- Arg Tyr Ser Gly Gln Glu Asp Ile Ala Ile Leu His Val Glu Asp Lys 50 55 60
- Ala Val His Pro Lys Asn Arg Asn Phe Lys Asp Tyr Thr Gly Ile Leu 70 75 80
 - Lys Ile Ala Ser Glu Ala Lys Glu Asn Glu Arg Ile Ser Ile Val Gly 85 90 95
- 60 Tyr Pro Glu Pro Tyr Ile Asn Lys Phe Gln Met Tyr Glu Ser Thr Gly 100 105 110
 - Lys Val Leu Ser Val Lys Gly Asn Met Ile Ile Thr Asp Ala Phe Val

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00	Ala	Gly 210		Lys	Pro	Ser	Gly 215	Glu	Ser	Thr	Arg	Gly		Ala	Val	туг

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Lys Lys Thr Ile Asn Ile Thr Leu Asp Met Asp Gly Arg Ile Pro Ile 5 Asn Val Trp Thr Gly Asp Ser Ile Ala Arg Ser Gly Arg Gly Thr Leu Ile Lys Leu Asn Leu Glu Asn Leu Asp Ala Leu Ser Lys Leu Ile Thr 10 Gly Glu Thr Ser Gly Met Leu Ala Glu Cys Val Ile Phe Leu Asn Glu 345 Ser Phe Asn Ile Ser Glu Asn Glu Asn Lys Asn Phe Ala Asp Arg Lys 15 Lys Gln Leu Ser Glu Gly Phe Lys Asp Lys Ile Asn Leu Phe Gln Leu 20 Glu Glu Met Glu Arg Thr Leu Ile Ser Lys Ile Asn Ser Leu Glu Glu Val Ala Asp Glu Thr Ile Glu Ser Ile Ser Ala Val Lys His Leu Leu 25 Pro Asp Phe Ala Leu Asp Ala Leu Lys Glu Arg Ile Asn Glu Leu Phe 425 Lys Gly Ile Lys Ser Phe Ile Glu Lys Val Tyr Asp Ser Ile Asp Asn 30 Glu Ile Leu Glu Ile Phe Lys Asn Ile Asp His Asp Phe Arg Asp Gly 455 35 Val Ser Glu Glu Met Met <210> 27 40 <211> 306 <212> PRT <213> Staphylococcus aureus <400> 27 45 Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu 50 Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys 55 Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val 60 Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys

5	Phe	Lys	Thr 115	Glu	Glu	Asp	Tyr	Lys 120	Ala	Glu	Lys	Leu	Leu 125	Ala	Pro	Tyr
J	Lys	Lys 130	Ala	Lys	Thr	Leu	Glu 135	Arg	Gln	Val	Tyr	Glu 140	Leu	Asn	Lys	Ile
10	Gln 145	Asp	Lys	Leu	Pro	Glu 150	Lys	Leu	Lys	Ala	Glu 155	Tyr	Lys	Lys	Lys	Leu 160
	Glu	Asp	Thr	Lys	Lys 165	Ala	Leu	Asp	Glu	Gln 170	Val	Lys	Ser	Ala	Ile 175	Thr
15	Glu	Phe	Gln	Asn 180	Val	Gln	Pro	Thr	Asn 185	Glu	Lуs	Met	Thr	Asp 190	Leu	Gln
20	Asp	Thr	Lys 195	Tyr	Val	Val	Tyr	Glu 200	Ser	Val	Glu	Asn	Asn 205	Glu	Ser	Met
	Met	Asp 210	Thr	Phe	Val	Lys	His 215	Pro	Ile	Lys	Thr	Gly 220	Met	Leu	Asn	Gly
25	Lys 225	Lys	Tyr	Met	Val	Met 230	Glu	Thr	Thr	Asn	Asp 235	Asp	Tyr	Trp	Ъўз	Asp 240
	Phe	Met	Val	Glu	Gly 245	Gln	Arg	Val	Arg	Thr 250	Ile	Ser	Lys	Asp	Ala 255	Lys
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35	Tyr	Asp	Ala 275	Ile	Val	ГÀЗ	Val	His 280	Val	Lys	Thr	Ile	Asp 285	Tyr	Asp	Gly
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	Asn	Arg	Ser	Tyr 20	Ala	Arg	Ala	Ser	Ala 25	Asn	Glu	Ile	Thr	Ser 30	Lуs	Thr
55	Val	Ser	Asn 35	Val	Ser	Arg	Thr	Gly 40	Asn	Asn	Ala	Asn	Val 45	Thr	Val	Thr
60	Val	Thr 50	Tyr	Gln	Asp	Gly	Thr 55	Thr	Ser	Thr	Val	Thr 60	Val	Pro	Val	Lys
00	His 65	Val	Ile	Pro	Glu	Ile 70	Val	Ala	His	Ser	His 75	Tyr	Thr	Val	Gln	Gly 80

Gln Asp Phe Pro Ala Gly Asn Gly Ser Ser Ala Ser Asp Tyr Phe Lys Leu Ser Asn Gly Ser Asp Ile Ala Asp Ala Thr Ile Thr Trp Val Ser 5 Gly Gln Ala Pro Asn Lys Asp Asn Thr Arg Ile Gly Glu Asp Ile Thr 120 10 Val Thr Ala His Ile Leu Ile Asp Gly Glu Thr Thr Pro Ile Thr Lys Thr Ala Thr Tyr Lys Val Val Arg Thr Val Pro Lys His Val Phe Glu 150 155 15 Thr Ala Arg Gly Val Leu Tyr Pro Gly Val Ser Asp Met Tyr Asp Ala Lys Gln Tyr Val Lys Pro Val Asn Asn Ser Trp Ser Thr Asn Ala Gln 20 His Met Asn Phe Gln Phe Val Gly Thr Tyr Gly Pro Asn Lys Asp Val 25 Val Gly Ile Ser Thr Arg Leu Ile Arg Val Thr Tyr Asp Asn Arg Gln Thr Glu Asp Leu Thr Ile Leu Ser Lys Val Lys Pro Asp Pro Pro Arg 30 Ile Asp Ala Asn Ser Val Thr Tyr Lys Ala Gly Leu Thr Asn Gln Glu Ile Lys Val Asn Asn Val Leu Asn Asn Ser Ser Val Lys Leu Phe Lys 35 265 Ala Asp Asn Thr Pro Leu Asn Val Thr Asn Ile Thr His Gly Ser Gly 40 Phe Ser Ser Val Val Thr Val Ser Asp Ala Leu Pro Asn Gly Gly Ile 295 Lys Ala Lys Ser Ser Ile Ser Met Asn Asn Val Thr Tyr Thr Thr Gln 45 Asp Glu His Gly Gln Val Val Thr Val Thr Arg Asn Glu Ser Val Asp Ser Asn Asp Ser Ala Thr Val Thr Val Thr Pro Gln Leu Gln Ala Thr 50 Thr Glu Gly Ala Val Phe Ile Lys Gly Gly Asp Gly Phe Asp Phe Gly 55 His Val Glu Arg Phe Ile Gln Asn Pro Pro His Gly Ala Thr Val Ala 375 Trp His Asp Ser Pro Asp Thr Trp Lys Asn Thr Val Gly Asn Thr His 395 60 Lys Thr Ala Val Val Thr Leu Pro Asn Gly Gln Gly Thr Arg Asn Val

Glu Val Pro Val Lys Val Tyr Pro Val Ala Asn Ala Lys Ala Pro Ser Arg Asp Val Lys Gly Gln Asn Leu Thr Asn Gly Thr Asp Ala Met Asn 5 Tyr Ile Thr Phe Asp Pro Asn Thr Asn Thr Asn Gly Ile Thr Ala Ala 455 10 Trp Ala Asn Arg Gln Gln Pro Asn Asn Gln Gln Ala Gly Val Gln His Leu Asn Val Asp Val Thr Tyr Pro Gly Ile Ser Ala Ala Lys Arg Val 490 15 Pro Val Thr Val Asn Val Tyr Gln Phe Glu Phe Pro Gln Thr Thr Tyr Thr Thr Thr Val Gly Gly Thr Leu Ala Ser Gly Thr Gln Ala Ser Gly 20 Tyr Ala His Met Gln Asn Ala Thr Gly Leu Pro Thr Asp Gly Phe Thr 25 Tyr Lys Trp Asn Arg Asp Thr Thr Gly Thr Asn Asp Ala Asn Trp Ser 550 Ala Met Asn Lys Pro Asn Val Ala Lys Val Val Asn Ala Lys Tyr Asp 30 Val Ile Tyr Asn Gly His Thr Phe Ala Thr Ser Leu Pro Ala Lys Phe 585 Val Val Lys Asp Val Gln Pro Ala Lys Pro Thr Val Thr Glu Thr Ala 35 600 Ala Gly Ala Ile Thr Ile Ala Pro Gly Ala Asn Gln Thr Val Asn Thr 40 His Ala Gly Asn Val Thr Thr Tyr Ala Asp Lys Leu Val Ile Lys Arg 630 635 Asn Gly Asn Val Val Thr Thr Phe Thr Arg Arg Asn Asn Thr Ser Pro 650 45 Trp Val Lys Glu Ala Ser Ala Ala Thr Val Ala Gly Ile Ala Gly Thr 665 Asn Asn Gly Ile Thr Val Ala Ala Gly Thr Phe Asn Pro Ala Asp Thr 50 Ile Gln Val Val Ala Thr Gln Gly Ser Gly Glu Thr Val Ser Asp Glu 55 Gln Arg Ser Asp Asp Phe Thr Val Val Ala Pro Gln Pro Asn Gln Ala Thr Thr Lys Ile Trp Gln Asn Gly His Ile Asp Ile Thr Pro Asn Asn 730 60 Pro Ser Gly His Leu Ile Asn Pro Thr Gln Ala Met Asp Ile Ala Tyr 740 745

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	Val 785	Thr	Leu	Asp	Ala	Gln 790	Thr	Gly	Lys	Val	Thr 795	Phe	Asn	Ala	Asn	Thr 800
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15	His	Ser	Val	Ser 820	Ser	Asn	Pro	Ser	Thr 825	Leu	Thr	Ala	Pro	Ala 830	Ala	His
15	Thr	Val	Asn 835	Thr	Thr	Glu	Ile	Val 840	Lys	Asp	Tyr	Gly	Ser 845	Asn	Val	Thr
20	Ala	Ala 850	Glu	Ile	Asn	Asn	Ala 855	Val	Gln	Val _.	Ala	Asn 860	Lys	Arg	Thr	Ala
	Thr 865	Ile	Lys	Asn	Gly	Thr 870	Ala	Met	Pro	Thr	Asn 875	Leu	Ala	Gly	Gly	Ser 880
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	Gln 945	Ile	Asn	Thr	Ala	Lys 950	Thr	Glu	Ala	Gln	Gln 955	Val	Ile	Asn	Asn	Glu 960
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- -	Asp		Thr L075	Ala	Asp	Thr		Ala L080	Leu	Glu	Gln		Val 1085	Gln	Gln	Leu

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20	Asp G 1185	ly	Met	Thr		Ser L190	Ser	Ile	Gln		Tyr L195	Glu	Asn	Ala		Arg 200
	Ala G	ly	Gln		GLu l205	Ser	Thr	Asn		Gln .210	Asn	Val	Ile		Asn 1215	Gly
25	Asp A	la		Asp 220	Gln	Gln	Ile		Ala 1225	Glu	Lys	Thr		Val 230	Glu	Glu
20	Lys T		Asn 235	Ser	Leu	Lys		Ala 1240	Ile	Ala	Gly		Thr L245	Pro	Asp	Leu
30	Ala P	ro 50	Leu	Gln	Thr		Lys l255	Thr	Gln	Leu		Asn 1260	Asp	Ile	Asp	Gln
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	Thr S		Thr 395	Ala	Asn	Gln		Lys .400	Ser	Asp	Leu		His 1405	Ala	Arg	Gln
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	Glu 142		Ser	Ile		Gln 1430	Pro	Thr	Asp		Thr 1435	Gly	Met	Thr		Ala 1440
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15		Arg 1490	Gln	Gly	Leu		Leu 1495	Asp	Arg	Gln		Ala 1500	Leu	Thr	Thr	Leu
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45	Val 1985		Ser	Ala		Asn 1990	Asn	Leu	Asp		Thr .995	Arg	Leu	Leu		Gln 2000
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13	Ala	Ser		Gln 2180	Asn	Gly	Ile		Asn 2185	Glu	Ser	Gln		Lys 2190	Ser	Ser
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JU	Val	Gln		Asn 2420	Ala	Thr	Glu	Leu 2	Asn 2425	Thr	Ala	Met		Thr 2430	Leu	Lys

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‡ 0	Thr	Leu	Ser		Leu 2645	Thr	Asn	Asn		Lys 2650	Ser	Ala	Ile		Ser 2655	Gln
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+3		0> 29														
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50	Ser		35 Ser	Asn	Glu	Ser	Lys	40 Ser	Asn	Asp	Ser	Ser	45 Ser	Val	Ser	Ala
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Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu 5 Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr 10 Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp 15 Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp 485 490 20 <210> 30 25 <211> 541 <212> PRT <213> Staphylococcus aureus <400> 30 30 Asp Gln Tyr Leu Leu Glu Arg Lys Lys Ser Gln Tyr Glu Asp Tyr Lys Gln Trp Tyr Ala Asn Tyr Lys Lys Glu Asn Pro Arg Thr Asp Leu Lys 35 Met Ala Asn Phe His Lys Tyr Asn Leu Glu Glu Leu Ser Met Lys Glu Tyr Asn Glu Leu Gln Asp Ala Leu Lys Arg Ala Leu Asp Asp Phe His 40 Arg Glu Val Lys Asp Ile Lys Asp Lys Asn Ser Asp Leu Lys Thr Phe 45 Asn Ala Ala Glu Glu Asp Lys Ala Thr Lys Glu Val Tyr Asp Leu Val Ser Glu Ile Asp Thr Leu Val Val Ser Tyr Tyr Gly Asp Lys Asp Tyr 50 Gly Glu His Ala Lys Glu Leu Arg Ala Lys Leu Asp Leu Ile Leu Gly 120 Asp Thr Asp Asn Pro His Lys Ile Thr Asn Glu Arg Ile Lys Lys Glu 55 Met Ile Asp Asp Leu Asn Ser Ile Ile Asp Asp Phe Phe Met Glu Thr Lys Gln Asn Arg Pro Lys Ser Ile Thr Lys Tyr Asn Pro Thr Thr His Asn Tyr Lys Thr Asn Ser Asp Asn Lys Pro Asn Phe Asp Lys Leu Val

180 185 190 Glu Glu Thr Lys Lys Ala Val Lys Glu Ala Asp Asp Ser Trp Lys Lys 200 5 Lys Thr Val Lys Lys Tyr Gly Glu Thr Glu Thr Lys Ser Pro Val Val Lys Glu Glu Lys Lys Val Glu Glu Pro Gln Ala Pro Lys Val Asp Asn 10 Gln Gln Glu Val Lys Thr Thr Ala Gly Lys Ala Glu Glu Thr Thr Gln 15 Pro Val Ala Gln Pro Leu Val Lys Ile Pro Gln Gly Thr Ile Thr Gly Glu Ile Val Lys Gly Pro Glu Tyr Pro Thr Met Glu Asn Lys Thr Val 20 Gln Gly Glu Ile Val Gln Gly Pro Asp Phe Leu Thr Met Glu Gln Ser 295 300 Gly Pro Ser Leu Ser Asn Asn Tyr Thr Asn Pro Pro Leu Thr Asn Pro 25 Ile Leu Glu Gly Leu Glu Gly Ser Ser Ser Lys Leu Glu Ile Lys Pro 330 30 Gln Gly Thr Glu Ser Thr Leu Lys Gly Thr Gln Gly Glu Ser Ser Asp Ile Glu Val Lys Pro Gln Ala Thr Glu Thr Thr Glu Ala Ser Gln Tyr 35 Gly Pro Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr Val Lys Tyr Arg Asp Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly Thr Phe Gly Tyr 40 Glu Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn 45 Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr 425 Tyr Lys Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Ala 440 50 Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln Asn Lys Pro Ser Lys Thr Asn Ala Tyr Asn Val Thr Thr His Gly Asn Gly Gln Val Ser 55 Tyr Gly Ala Arg Gln Ala Gln Asn Lys Pro Ser Lys Thr Asn Ala Tyr 60 Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro 505 Thr Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn Val Thr Thr His

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Met Ile Ser Arg Asp Val Ser Glu Tyr Met Ile Thr Lys Glu Glu Ile 275 280 285

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 - His Asn Leu Tyr Gly Asn Met Gly Ser Gly Thr Ile Val Ile Lys Met 305 310 315 320
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INTERNATIONAL SEARCH REPORT

International Application No PCT/GB 01/02685

			PC	1/6B 01/02685
A CLASS IPC 7	C12N15/31 C12N15/63 G01N3 C07K16/12 C12N5/12 A61K3		C07K14/31	A61K39/085
According	to International Patent Classification (IPC) or to both national class	ification and IP	C	
	SEARCHED			
Minimum d	locumentation searched (classification system followed by classifi C12N G01N C07K A61K	cation symbols)		
Documenta	ation searched other than minimum documentation to the extent th	at such docume	ints are included in t	he fields searched
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	tata base consulted during the international search (name of data of the part	base and, whe	re practical, search (erms used)
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT			
Category °	Citation of document, with indication, where appropriate, of the	relevant passat	ges	Relevant to claim No.
Х	ARIFUR RAHMAN ET AL.: "Gamma-I genes in the same family with I	ukF and	1	1-9, 18-48
A	lukS genes in methicillin resistaphylococcus aureus" BIOSCIENCE BIOTECHNOLOGY BIOCHE vol. 57, no. 7, 1993, pages 123 XP002177747 TOKYO JP the whole document WO 99 50418 A (NEUTEC PHARMA PL 7 October 1999 (1999-10-07) the whole document	EMISTRY., 34-1236,		1-9, 18-49
Furt	her documents are listed in the continuation of box C.	X Pa	tent family members	are listed in annex.
° Special ca	ntegories of cited documents:	"T" later doc	xment published aft	er the International filing date
consid "E" earlier of filing d		or prior cited to inventi "X" docume cannot	rity date and not in co o understand the prin on int of particular relev: be considered nove	onflict with the application but ciple or theory underlying the ance; the claimed invention for cannot be considered to
which citation "O" docume other i "P" docume	ent published prior to the international filing date but	then the document is taken alone ance; the claimed invention rolve an inventive stop when the one or more other such docu- eing obvious to a person skilled		
	nan the priority date claimed actual completion of the international search		nt member of the same	me patent family ational search report
	8 September 2001	DAWG	19.11.	•
Name and r	nailing address of the ISA	*Authoriz	zed officer	
	European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 661 epo nl, Fax: (+31-70) 340-3016	M	IONTERO LOPI	EZ B.

INTERNATIONAL SEARCH REPORT

International application No. PCT/GB 01/02685

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. X Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 26-32 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Light Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
1. As all required additional search fees were timely paid by the applicant, this international Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the Invention first mentioned in the claims; it is covered by claims Nos.: Partially 1-9, 18-49
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Partially 1-9, 18-49

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:1, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

2. Claims: Partially 1-9, 18-49

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:2, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

3. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:3, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

4. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:4, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

5. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:5, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

6. Claims: Partially 1-9, 18-48

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:6, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

7. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:7, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

8. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:8, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

9. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of

SEQ ID NO:9, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

10. Claims: Partially 1-9, 18-48

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:10, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

11. Claims: Partially 1-9, 18-48

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:11, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

12. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:12, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

13. Claims: Partially 1-9, 19-46

Staphylococcus aureus antigen encoded by a DNA sequence of SEQ ID NO:13, DNA sequence and variants thereof; vectors and host cells comprising the same and their use for the production of the polypeptide; vaccine comprising the

antigen and its use in immunisation; antibodies directed to the antigen and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament; use of the polypeptides for preparing a hybridoma cell-line.

14. Claims: 10-17, and partially 24-46

Method to identify antigenic polypeptides by transfecting a pathogenic organism gene library into a host cell and contacting the expressed polypeptides with autologous antisera from an animal infected with the pathogenic organism; polypeptides so obtained, vaccines comprising the antigenic polypeptides and use in immunisation; antibodies directed to the antigenic polypeptides and vectors and hybridoma cells for their production; use of the antibodies for the manufacture of a medicament.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No PCT/GB 01/02685

Patent document cited in search report		Publication date		Patent family member(s)	Publication date	
WO 9950418	A	07-10-1999	AU EP WO	3156699 A 1068328 A1 9950418 A1	18-10-1999 17-01-2001 07-10-1999	